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Multiple Trait Evaluation of Bulls for Calving Ease

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ABSTRACT

Evaluation of bulls for calving difficulty of their calves by a multiple trait, mixed model procedure seems appropriate for a number of reasons. Average calving ease scores and their variances and heritabilities differ according to sex of calf and parity of mother. The multiple trait procedure automatically accounts for differences in averages, variances, and heritabilities. The procedure also allows for the magnitude of herd-year-season effects to be different for four traits as defined by calving difficulty scores when measured on: male birth by a heifer, female birth by a heifer, male birth by a cow, and female birth by a cow. Covariances among herd effects for the four traits are used in the multiple trait procedure to prevent certain comparisons within herd from being lost. Records on all four traits are weighted properly to evaluate sires for calving ease for all sex-of-calf and parity-of-cow combinations. Evaluations for the four traits can be weighted to obtain a single evaluation for expected fraction of acceptable births.

Computing costs do not seem prohibitive. The procedure, however, does not take advantage of ordering of categorical responses or of an underlying continuous biological distribution as would threshold models.

INTRODUCTION

Most evaluations of bulls for difficulty of birth of their calves have been on births scored on a linear scale; often the scores are 1 to 5 from no difficulty to extreme difficulty (1, 2, 4, 15, 16, 18, 20). Measurements have been

treated as a single continuous variable with discrete scoring. Analyses on such an "as scored" basis have adjusted for various identifiable factors that influence the difficulty of birth such as sex of calf, parity of mother, and size of mother.

Exceptions to the "as scored" analyses have included various transformations that attempt to normalize the multinomial scoring (2, 8, 9, 10, 18, 19, 21). After transformation the scores have been analyzed as a single trait. Harville and Mee (12) and Gianola and Foulley (11) have proposed methods that assume an underlying normal distribution in which threshold points corresponding to the categories are estimated jointly along with fixed effects such as sex of calf and parity of mother and random effect of sire of calf. Quaas and Van Vleck (17) proposed another method, which was used by Cady (4). Each measurement is considered a vector of observations of zeros and a single one that corresponds to the category scored for the birth. This method of bull evaluation is a special case of mixed model evaluation for multiple traits with the final bull evaluations corresponding to predictions of frequencies of future births being scored in each of the several categories. Because variance-covariance matrices depend on frequencies in each of the categories, the procedure requires a separate analysis when frequencies are different. For example, frequencies are different for many sex of calf and parity of mother combinations.

The purpose of the current study was to extend the categorical multiple trait approach to the case where each category of each sex of calf-parity of mother combination is a separate trait. For example, with five categories, two sexes, and three parities, the total number of traits would be 30. Difficulties in estimating covariances among traits led to the compromise of a simpler approach, which is described here. The extension to the complete procedure is straightforward except for requiring more computing time.

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EVALUATION PROCEDURE

The model is a multiple trait random model with scores for each sex of calf-parity of mother combination a separate trait. As described here, measurements can be as scored (i.e., 1 to 5) or acceptable-unacceptable (i.e., 1 or 0, depending on what scores are considered acceptable). The current National Association of Animal Breeders (NAAB) summary considers scores of 4 and 5 to be unacceptable and scores of 1, 2, and 3 to be acceptable, although the analysis is on an as-scored basis (2).

Evidence for considering dystocia scores for different sex of calf-parity of mother combinations as separate traits can be obtained from any analysis of calving difficulty (e.g., 2, 3, 5, 6, 7). For example, a sample of 87,000 scores collected by Eastern Artificial Insemination Cooperative (EAIC) yielded the estimates in Table 1 for measurements on an acceptable-unacceptable basis and on an as-scored basis (7). Means, variances, and heritabilities all differ from subclass to subclass. Analysis of NAAB data as-scored have shown similar patterns (2, 16).

The NAAB procedure (2) normalizes variances of scores for parity of mother but not for sex of calf. That mixed model procedure assumes a single trait and, thus, can include only an estimate of heritability averaged over all sex-parity combinations. The effect of using an average sire component of variance and different residual variances for each parity is in Table 2. Heritability is effectively smallest for the first parity that has the largest residual variance. In fact, however, when heritability was estimated separately for each parity, the

estimate was largest for first parity (2). The proposed procedure allows for different variances, different sire effects, and genetic correlations of less than one for different sex of calf-parity of mother combinations.

The NAAB procedure considers sex of calf and parity of mother effects to be fixed. Further, the effect associated with herd-year-season (HYS) of calving is considered fixed and of the same magnitude for each sex-parity combination. The proposed procedure adjusts for effects of sex of calf-parity of mother by estimating the mean for each combination. The proposed procedure considers that HYS effects are random, that magnitudes of HYS effects can be different for each sex-parity combination, and that HYS effects may not be perfectly correlated between, for example, male-first parity births and female-later parity births.

The NAAB procedure converts the sire solutions for as-scored data to an expected fraction of unacceptable first parity births (4's and 5's). The proposed procedure directly predicts the fraction of acceptable births (or fraction unacceptable) for each sex-parity combination if the measurements are acceptable-unacceptable. These then can be weighted by the expected frequencies of sex-parity calvings to obtain the predicted fraction of acceptable first parity births or fraction of acceptable all parity births. For example, the fraction of acceptable male-first parity births and female-first parity births could be averaged to obtain the expected fraction of first parity births under the assumption (not quite true) that bull and heifer calves are born equally frequently. If the proposed procedure is applied

TABLE 1. Evidence for considering scores for difficulty of different sex of calf-parity of mother combinations as different traits (7).

Sex of calf/ parity of mother	Scored as 1 = acceptable (a 1, 2, or 3) or 0 = unacceptable (a 4 or 5)			As scored, 1 to 5		
	Mean	Variance	Heritability	Mean	Variance	Heritability
Male/first (M1)	.87	.10	.16	1.86	1.29	.27
Female/first (F1)	.94	.06	.16	1.51	.93	.23
Male/later (M2)	.96	.04	.05	1.37	.67	.12
Female/later (F2)	.98	.02	.006	1.21	.41	.05

TABLE 2. Residual variances used to standardize the variances in the calving difficulty analysis¹ and the effect on the effective heritability of using a single sire component of variance.

Parity	Residual variance	Heritability	
		As used	As estimated
1	1.44	.05	.17
2	.78	.10	.08
3	.65	.12	.05

¹Adapted from Berger and Freeman (2).

to as-scored data, then some method must be used to convert to acceptable-unacceptable as does the NAAB procedure.

The proposed model is limited to four traits for simplicity although it could be extended to more sex of calf-parity of cow combinations if necessary. The four traits correspond to scores on: 1) male-first parity births, M1; 2) female-first parity births, F1; 3) male-later parity births, M2; and 4) female-later parity births, F2.

The multiple trait random model is standard (13, 14) except that the residuals (e) are independent:

$$\begin{aligned}
 y &= X\mu + Wh + Zs + e && \text{with} \\
 \mu &= (\mu_{M1} \mu_{F1} \mu_{M2} \mu_{F2})' \\
 h &= (h'_1 \dots h'_f) \\
 h_i &= (h_{iM1} h_{iF1} h_{iM2} h_{iF2})' \\
 s &= (s'_1 \dots s'_r) \\
 s_j &= (s_{jM1} s_{jF1} s_{jM2} s_{jF2})'
 \end{aligned}$$

$$S = \begin{bmatrix} a_{11}S_0 & a_{12}S_0 & \cdot & \cdot & \cdot & a_{1r}S_0 \\ & a_{22}S_0 & \cdot & \cdot & \cdot & a_{2r}S_0 \\ & & \cdot & \cdot & \cdot & \\ & & & \cdot & \cdot & \\ & & & & \cdot & \\ \text{Symmetric} & & & & & a_{rr}S_0 \end{bmatrix} \quad \text{if } A \neq I.$$

where y is the vector of N observations, μ is the vector of means associated with the four traits, h_i is the vector of HYS effects associated with the four traits in the *i*th HYS (*f*, HYS's), s_j is the vector of bull effects associated with the four traits for calves sired by the *j*th bull (*r*, sires), e is the vector of residual effects corresponding to y with each individual element, e_{ijk} being the residual effect associated with the *k*th calf of the *j*th bull born in the *i*th HYS and which will be an M1, F1, M2, or an F2 birth, and X, W, and Z are incidence matrices associating each measurement with the corresponding mean, HYS, and sire effects.

Further:

$$E(y) = X\mu$$

$$V \begin{bmatrix} h \\ s \\ e \end{bmatrix} = \begin{bmatrix} I^*H_0 & 0 & 0 \\ 0 & A^*S_0 & 0 \\ 0 & 0 & R \end{bmatrix} = \begin{bmatrix} H & 0 & 0 \\ 0 & S & 0 \\ 0 & 0 & R \end{bmatrix}$$

where I is an identity matrix of order the number of herd-year-seasons, * indicates the right direct product operation, A is the numerator relationship matrix among the sires, and H_0 is the variance-covariance matrix of HYS effects for the four traits in the same herd-year-season with effects ordered as in h_i .

Similarly, the variance-covariance matrix of bull effects for the four traits for calves of a bull is S_0 :

$$S = V(s) = \begin{bmatrix} S_0 & & & 0 \\ & \cdot & & \\ & & \cdot & \\ 0 & & & S_0 \end{bmatrix}$$

if $A=I$ (i.e., bulls assumed unrelated) and:

The variance-covariance matrix of residuals is assumed to be diagonal because all observations within an HYS are independent on a sampling basis, as each calf can be measured on only one trait whereas in most multiple trait models each animal is likely to have measurements on many or all traits. The same cow may have more than one calf. Any residual

covariance between measurements on calves of the same cow was ignored.

Thus, $R = V(e)$ is a diagonal matrix of order N with each element, the residual variance for the corresponding sex-parity of birth: i.e., elements are σ_{M1}^2 or σ_{F1}^2 or σ_{M2}^2 or σ_{F2}^2 .

The usual mixed model equations for this multiple trait situation are:

$$\begin{bmatrix} W'R^{-1}W+H^{-1} & & & \\ & W'R^{-1}X & & \\ & X'R^{-1}X & & \\ & & W'R^{-1}Z & \\ & & X'R^{-1}Z & \\ & & Z'R^{-1}Z+S^{-1} & \end{bmatrix} \begin{bmatrix} \hat{h} \\ \hat{\mu} \\ \hat{s} \end{bmatrix} = \begin{bmatrix} W'R^{-1}y \\ X'R^{-1}y \\ Z'R^{-1}y \end{bmatrix}$$

Symmetric

The equations often are solved after HYS equations are absorbed a vector (h_i) at a time as the other coefficients are collected.

A property of this special case of multiple trait evaluation should be noted. For absorption of any HYS vector, for example h_1 , the diagonal block for the absorption is:

$$\begin{bmatrix} n_1 \cdot M1 / \sigma_{M1}^2 & 0 & 0 & 0 \\ 0 & n_1 \cdot F1 / \sigma_{F1}^2 & 0 & 0 \\ 0 & 0 & n_1 \cdot M2 / \sigma_{M2}^2 & 0 \\ 0 & 0 & 0 & n_1 \cdot F2 / \sigma_{F2}^2 \end{bmatrix} + \begin{bmatrix} H_0^{-1} \end{bmatrix}$$

where $n_1 \cdot M1$, etc., are the numbers of observations on the four traits in HYS 1.

When HYS effects are considered random with variance-covariance matrix, H_0 , for effects in the same HYS, comparisons are not lost when, for example, one bull has an M1 calf, another bull has an F2 calf, and those are the only two births in that HYS. If HYS effects are considered fixed, then absorption would eliminate such comparisons.

APPLICATION

The procedure was applied to an edited set of 87,070 calving difficulty scores of calves of Holstein cows by 484 Holstein bulls in 12,867 HYS collected by EAIC from 1974 through

1981. Until 1980, calving difficulty information was reported on all calvings for their own herds by individual dairy producers selected by EAIC area managers. In 1980 and 1981 EAIC technicians collected information only on calves of young sampling bulls. Season 1 included calendar months April through September, and season 2 included calendar months October through December and the subsequent 3 mo of the next year. Editing was to eliminate duplicate records, multiple births, and scores outside the permitted range. Malpresentations were not recorded so could not be eliminated. An additional 88 bulls without calves were included from calculation of the inverse of the relationship matrix using only sires (13). A major difficulty arose in that estimates of some

elements of the variance-covariance matrices were outside the biological limits (7). For example, some of the HYS variances were negative, and some of the correlations exceeded one. Residual variances were those reported by Edlin and Van Vleck (7) of .10143, .05877, .03804, and .01942 for M1, F1, M2, F2 scores. Variances were estimated from the same data set with Henderson's method 1 for a model including HYS and sire effects. The HYS and sire covariances were estimated similarly from products of subclass means for the four types of birth.

The variance-covariance matrices that were used for HYS and sire effects are in Table 3. The variance component for HYS effects was arbitrarily set at .05 of the residual variance for that trait if the estimate from the data was smaller than that. The component of variance for sire effects for F2 scores was set at .005 of the residual variance, which corresponds to a heritability of .02 rather than the .006 estimated from the data. Covariances were computed from assigned arbitrary correlations when estimated correlations were outside biological limits. Correlations between M1 and F1 scores and between M2 and F2 scores were rounded from estimates and were higher than correlations arbitrarily assigned between traits that did not seem as closely related by parity. Before this procedure would be implemented, better estimates of variances and covariances would be desirable. Because intuitively covariances would be positive, assigning zero covariances does not seem desirable when estimates of correlations

are greater than one. Similarly correlations across parities would be expected to be smaller than correlations within parity. Care must be taken to ensure that variance-covariance matrices are positive definite.

The computing strategy was:

- 1) HYS equations were absorbed one HYS block at a time as the coefficients were collected in half-stored form and written on tape.
- 2) Coefficients were sorted in order.
- 3) Coefficients with the same coded identification were summed and written on tape in full-stored form.
- 4) Summed coefficients were sorted.
- 5) Equations were solved by block iteration, where each block after the first corresponded to the four equations for each bull with the first block corresponding to the four μ equations.
- 6) The initial estimates for the μ solution vector were obtained as the product of the inverse of the corresponding diagonal block of coefficients and the corresponding right-hand sides. The initial estimates for the sire solution vectors were zeros.
- 7) The solution vector was updated after each block of each round as usually is done with Gauss-Seidel iteration. Relaxation was not used as there was no way of knowing what relaxor would be optimum.

Convergence was achieved in four rounds. The criterion for convergence was for the square root of the sum of squares of residuals of the regenerated right-hand sides from the original right-hand sides (the residual Euclidean

TABLE 3. Variance-covariance matrices of herd-year-season, H_0 , and sire, S_0 , effects for four calving difficulty traits (correlations in parentheses).

H_0				S_0			
.00734	.00395	.00224	.00133	.00421	.00308	.00104	.00039
	(.85)	(.60)	(.50)		(.95)	(.70)	(.60)
	.00294 ¹	.00118	.00101		.00250	.00057	.00025
		(.50)	(.60)			(.50)	(.50)
Symmetric		.00190 ¹	.00109	Symmetric		.00052	.00020
			(.80)				(.89)
			.00097 ¹				.00010 ²

¹.05 σ^2 , where σ^2 is the residual variance for that type of birth.

².005 σ^2 , where σ^2 is the residual variance for that type of birth.

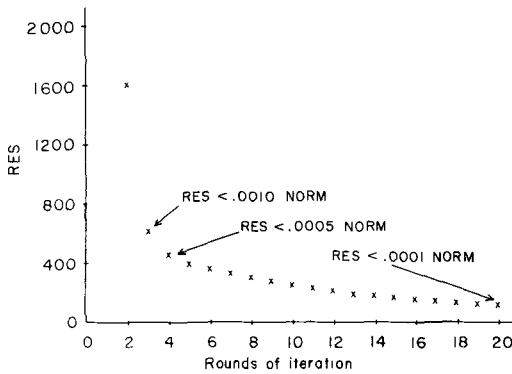


Figure 1. Convergence of solutions. For equations $Ax = r$, $NORM = (r'r)^{.5}$ and, at the k^{th} round, $RES = [(r - Ax^k)'(r - Ax^k)]^{.5}$.

norm) to be less than .0005 of the Euclidean norm of the original right-hand sides. The procedure is as described in Figure 1, which also illustrates rate of convergence.

The residual norm is approximated as a by-product of the block by block iteration procedure and thus lags the true residual norm by about one-half a round of iteration, i.e., is an underestimate of the true residual norm. For Gauss-Seidel iteration during the n^{th} round of iteration of N equations, $Ax = r$, the solution for the i^{th} equation is obtained as:

$$x_i^n = x_i^{n-1} + (r_i - \sum_{j=1}^{i-1} a_{ij}x_j^n - a_{ii}x_i^{n-1} - \sum_{j=i+1}^N a_{ij}x_j^{n-1})/a_{ii}$$

The residual term in brackets is the approximation used for the residual for the i^{th} equation. The actual residual would be calculated after all solutions for round n were obtained as:

$$(r_i - \sum_{j=1}^{i-1} a_{ij}x_j^n - a_{ii}x_i^n - \sum_{j=i+1}^N a_{ij}x_j^n)$$

This description is in terms of single equations, but the same principle was applied to the block iteration actually used. In that case x_i and r_i become vectors of length 4, the a_{ij} and a_{ij} are diagonal and off-diagonal blocks of dimension 4 by 4, and N is the number of sires plus 1 for the mean vector. Comparison of the solutions for .0005 of the norm and .0001 of

the norm revealed few significant changes in bull evaluations for the average of M1 and F1. Of 273 bulls with 40 or more calves, only 2 changed by as much as .006, 9 by .005, 22 by .004, and 32 by .003.

The sire comparison vector, for example, for bull j is:

$$SC_j = \hat{\mu} + \hat{s}_j$$

The elements of this vector predict the fraction of future calves of bull j that will be scored acceptable for M1, F1, M2, and F2. Sire comparisons depend on the mean vector. If means for the four traits change, then expected fractions of future progeny would change also.

These solutions can be weighted to obtain a combined solution. For example, if equal frequencies of male and female births are assumed, the expected fraction of acceptable first parity births would be:

$$SC_{j1} = .5(\hat{\mu}_{M1} + \hat{s}_{jM1}) + .5(\hat{\mu}_{F1} + \hat{s}_{jF1})$$

The expected fraction of acceptable births over all parities would be:

$$SC_{jALL} = PM1SC_{jM1} + PF1SC_{jF1} + PM2SC_{jM2} + PF2SC_{jF2}$$

where p_k are frequencies of births, which are M1, F1, M2, and F2. For the data set furnished by EAIC, these frequencies were .092, .083, .449, and .376. As pointed out by a reviewer, and others, the disproportionate sex ratios particularly for older cows may indicate a tendency to report only difficult births of which a higher proportion are males.

The procedure seems to be computationally efficient. No real effort was made to obtain efficient programs other than as described in the list of programs. All programs were written in Fortran except for a rapid assembly language subroutine for tape input and output routinely used in research programming at the New York Dairy Records Processing Laboratory. Some idea of the timing and tape requirements can be obtained from Table 4. Programs were run on an IBM 4341 with tape and disk input and disk sorts.

TABLE 4. Programs used in bull evaluations for calving difficulty.

Program	Records		Central processing unit time (min)
	Input	Output	
Absorb herd-year-season equations and collect half-stored coefficients	87,070	494,507 (blocks of 16 coefficients)	7.5
Sort 1	494,507	494,507	3.4
Sum and full-store like coefficients	494,507	768,676 (individual coefficients)	2.6
Sort 2	768,676	768,676	3.3
Block iteration (4 rounds, first from tape, 3 on disk)	768,676	484 (vectors of solutions)	3.5
Total			20.3

The procedure can be modified easily to add new data because previous data ordinarily are not corrected for errors and because new data include only new herd-year-seasons. The new data are run essentially through step 4, at which time the new coefficients after absorption are merged with the previous coefficients. Thus, any major increase in the timings will be in the iteration program as more sires are added to the system.

The sire comparisons are explained easily. As an example, for bulls with at least 40 calves, comparisons for the best and worst three bulls ranked on average predicted future frequency of acceptable births to first parity heifers are in Table 5. Predictions range from .684 to .985 for all first parity births and from .608 to .962 for male calves born to first parity heifers. The procedure does not guarantee that predictions of acceptable births will not exceed 1.00 even

TABLE 5. Lowest three and highest three comparisons for first parity births for bulls with 40 or more calves born.

	No. of calves	Expected fraction acceptable: 1's, 2's, or 3's					
		Male first parity	Female first parity	Male later parity	Female later parity	First ¹ parity	All ² parities
High	1	.962	1.007	.992	.996	.985	.992
	2	.945	.995	.998	.995	.970	.987
	3	.943	.997	.986	.995	.970	.986
Average	87,070	.880	.950	.967	.987	.915	.965
Low	3	.774	.844	.935	.972	.794	.924
	2	.711	.851	.894	.960	.781	.898
	1	.608	.760	.883	.953	.684	.874

¹ Sire comparisons for M1 and F1 weighted equally.

² Sire comparisons weighted by frequencies of sex-parity combinations (M1, .092; F1, .083; M2, .449; F2, .376).

when correct variances and covariances are known. Similarly the NAAB procedure could produce negative estimates of frequencies of unacceptable births.

DISCUSSION AND CONCLUSIONS

The multiple trait procedure allows for HYS and sire effects of unequal magnitudes for different types of births. Computing costs appear reasonable, the procedure allows for efficient updating with new data, and the results of the evaluation are easy to understand.

If an acceptable birth were defined differently, for example, as a 1 (no difficulty), the procedure requires only a change in the variance-covariance matrices in the collection-absorption program.

There may be some question of whether calving difficulty is a different trait for different sex-parity groups, but different means, variances, and heritabilities argue for treating sex-parity groups as separate traits.

Acceptable-unacceptable measures of difficulty imply a score of 1 equal to a score of 3 and a score of 4 equal to a score of 5. Thus, some information is lost on conversion to acceptable-unacceptable. The extended multiple trait categorical procedure would consider such information. The procedures of Harville and Mee (12) and Gianola and Foulley (11) may be even more appropriate, because threshold points along an underlying assumed normal distribution are estimated jointly. The amount of computing required appears greater for their procedures.

Another question is whether HYS effects should be considered fixed or random. Considering them to be random allows across sex-parity comparisons whereas considering them to be fixed does not. However, an association of certain bulls and certain herds (based on calving difficulty) can lead to biased evaluation. Treating HYS as fixed effects adjusts for such an association. This problem seems more likely for bulls that have been around for awhile, because each crop of new bulls will have essentially no information to use for selection by different herds.

The more difficult problem appears to be in obtaining estimates of the variance-covariance matrices. The problem is even more acute for the categorical multiple trait procedure.

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